

; LOCATION: 1, 2, 1675, 1676, 1677, 1678, 1679, 1680, 1681
 ; OTHER INFORMATION: n - A,T,C or G
 US-10-198-846-13222

Alignment Scores:

Pred. No.:	1,85e-211	length:	1681
Score:	1799.00	Matches:	350
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-745-506-37 (1-350) x US-10-198-846-13222 (1-1681)

OY	1	MetaspheulysalaleuLeuSerSerleuanspPhealaSerleuSerPhealGlu	20
Db	239	ATGATATTGAAGGCTCTCCTTTCTTCTCTGAAATGACTTTGCATCCCTCGTGGCTGAG	298
OY	21	SerTrpaspasValGlyLeuLeuValGluProSerProProIsthrValAsnThrLeu	40
Db	299	AGTTGGGCAAAATGTTGGATTACTGGTGGAAACCAAGCCACACATACTGTAATAATCACTC	358
OY	41	PheleuthrAsnaapleuThrGluGluValMetIuGluValLeuGluInlysAlaAsp	60
Db	359	TTCTGTGACCAATGACCTGACTGAGAGAAAGTGTGAGAGGGTGCTGCAGAAAGAGGAC	418
OY	61	LeuIleuSerTYrHisProProIlePheArgProMetIysArgIleThrTrpAsnThr	80
Db	419	CTCATTTCTCTTCACATCCGCCATATCTCCGAGCCCATGAAAGGCAATACCTGGAAACACA	478
OY	81	TrpIysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTYrSerProHis	100
Db	479	TGGAGAGGAGCCCTGGGTGATCCGGGGCTTGAGAAACAGAGTGGATCTTCTTCCTCAT	538
OY	101	ThrIaIarYrAspAlaAlaProGluGlyValAsnaSnrPleuAlaIysGlyLeuGlyAla	120
Db	539	ACAGCCTATGATGCTGCGCCCGCCAGGGCTCAACAACGTGTGGCTAAAGGCTTGGAGCT	598
OY	121	CysThrSerArgProIleHisProSerIysAlaProAsnTYrProThrGluGlyAsnHis	140
Db	599	TGTACCTCCAGGCCCATACATCTTCCAAACCTCCCAATCCCTACAGAGGAAACCCAC	658
OY	141	ArgValGluPheAsnValAsnTYrThrGlnAspIleuAspIysValMetSerAlaValIys	160
Db	659	CGAGTAGAATTCACAGCTTAACCTAACCCCAAGACCTGGCAAAAGTACATGCTCGAGTGA	718
OY	161	GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluInThr	180
Db	719	GGAAATTGACGGGTGTTTCTGTCACTCTTTTCTCTGAGACTGGTAATGAGAACCAACA	778
OY	181	ArgIleAsnLeuAsnCysThrGlnIysAlaIleuMetGluValValAspPheLeuSerArg	200
Db	779	CGGATTAATTCGAANTGACTACAGAAAGGCTTGTATGACGAGGGTGAATTTCTTCCCGG	838
OY	201	AsnIysGluLeuTYrGlnIysThrGluIleLeuSerLeuGluIysProLeuLeuLeuHis	220
Db	839	AACAACAACTTTATCGAAGACGGAATTCGTGCACGAGGAAGCCCTTGCTCTACAT	898
OY	221	ThrGlyMetGlyArgLeuCysThrIleuAspGluSerValSerLeuAlaThrMetIleAsp	240
Db	899	ACTGGAAAGGACGGTTATGCAACACTGGATGAATCTGCTCCGGAACCATGATTTGAT	958
OY	241	ArgIleIysAlaGHisLeuIysLeuSerHisIleArgLeuAlaLeuGlyValGlyAlaThr	260
Db	959	CGAATTAATAAACACACTTAACCTATCTCATATTGCTTAAGCCCTTGGGGTGGGAGAACCC	1018
OY	261	LeuGluSerGluValIysValValAlaLeuCysAlaGlySerGlySerSerValLeuGluIn	280
Db	1019	TTAAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGTGGAGACGCGTCTGCAG	1078
OY	281	GlyValGluAlaAspLeuTYrLeuThrGlyIleuMetSerHisHisAspThrLeuAspAla	300
Db	1079	GGGTGTGGGGCTGACCTTACCTCAGAGTGAAGTCCATGCATGATACCTTGGAGTCT	1138

QY	301	AlaserclnglylleasnaVallleleucCysGlnHisserasnThrGluargGlyPheLeu	320
Db	1139	GCTTCCCAAGAAATAATGTCATCCTCTGTGAAACACAGCAACACTGGAAGGGGTTTCTT	1198
QY	321	SeraspLeuArgaspMetIleuAspSerHisIeuGlnAsnLysIleasnIleleuSer	340
Db	1199	TCTGACCTTCGAGATGAGCTGGATTCTCCACTTGGAGAAATGAATTAATTCCTAACA	1258
QY	341	GluThrAspArgaspProLeuGlnValVal	350
Db	1259	GAGACTGACAGAGGACCCCTCTTCAGGTGTA	1288

RESULT 2

```

US-10-177-900-10/c
: Sequence 10, Application US/10177900
: Publication No. US20030068787A1
:
: GENERAL INFORMATION:
: APPLICANT: Jackson, Jennifer L.
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Arvizu, Chandra
:
: TITLE OF INVENTION: AN ANTIBODY SPECIFICALLY BINDING CYCLOPHILIN-TYPE PEPTIDYL-PRO
:
: FILE REFERENCE: PF-0582-2 CIP
:
: CURRENT APPLICATION NUMBER: US/10/177,900
:
: CURRENT FILING DATE: 2002-06-20
:
: PRIOR APPLICATION NUMBER: 09/440,828
:
: PRIOR FILING DATE: 1999-11-15
:
: PRIOR APPLICATION NUMBER: 09/136,442
:
: PRIOR FILING DATE: 1998-08-19
:
: NUMBER OF SEQ ID NOS: 12
:
: SOFTWARE: PERL Program
:
: SEQ ID NO 10
:
: LENGTH: 2922
:
: TYPE: DNA
:
: ORGANISM: Mus musculus
:
: FEATURE:
:
: NAME/KEY: misc-feature
:
: OTHER INFORMATION: Incyte ID No. US20030068787A1 023075_Mm.3
:
: US-10-177-900-10

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Alignment Scores:	
Pred. No.:	1,92e-183
Score:	1575.00
Percent Similarity:	93.14%
Best Local Similarity:	86.29%
Query Match:	87.35%
DB:	14
	Gaps: 0

US-09-745-506-37 (1-350) x US-10-177-900-10 (1-2922)

QY	1	MetaspLeuNysAlaLeuLeuSerSerLeuAsnspPheAlaSerLeuSerPheAlaGlu	20
Db	1251	ATGGATCTGAAGGCTCTCTCTCTGCTCCCTTGAAATACCTTGGATCCCTCTCATTTGGCGAG	1192
QY	21	SerTrpAspAsnValIglYLeuLeuValIgluProSerProProHisTrhValAsnThrLeu	40
Db	1191	AGCTGGGCATATGGGATTTACTGGTGGAGCCAGCCACCCTTACTGTAAATAACCTC	1132
QY	41	PheLeuThrAsnAspLeuThrGluGluValMetIuGluValLeuGlnInlyValAlaAsp	60
Db	1131	TTCTGTGACCAATGACCTGTACGAGAGGCTCATGTGACGAGGCTTGTCCAAAGAGGCACAC	1072
QY	61	LeuIleLeuSerTrpHisProProIlePheArgProMetIysArgIleTrhTrpAsnThr	80
Db	1071	TTCAATTCCTCTCTACCATCCACCTATTTTCCGGCCCATGAAGCAATAAATCTGGAAAAAC	1012
QY	81	TrpIysGluArgLeuValIleArgAlaLeuIuAsnArgValIglYIleTrpSerProHis	100
Db	1011	TGGAGGAGTCTCTCGTGATCCGGGCTGTGAGAGAACAGATCGCTGTACTCTCCCCAC	952
QY	101	ThrAlaTrpAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla	120


```
RESULT 4
US-10-027-632-161386/c
; Sequence 161386, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161386
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161386

Alignment Scores:
Pred. No.: 1,87e-75 Length: 817
Score: 692.50 Matches: 175
Percent Similarity: 73.99% Conservative: 27
Best Local Similarity: 64.10% Mismatches: 60
Query Match: 38.49% Indels: 16
DB: 13 Gaps: 1

US-09-745-506-37 (1-350) x US-10-027-632-161386 (1-817)

OY 16 LeuserPheAlaGluSerTTrpAspAsnValGlyLeuValGluProSerProRoHis 35
DB CTCTATTGCTAAAGTTGTGACATATGAA-TTACTGGTGGAAACCAAGACATCAT 728
OY 36 ThrValAsnThrLeuPheLeuThrAsnAspLeuThrGluValMetGluValIleu 55
DB GCTATTAACACATC-TTCCAGACCAATGACTGAGGAGTGATGGAGAGGTGCTG 669
OY 56 GluIysLysAlaAspLeuIleLeuSerTyrHisProProIlePheArgProMetLysArg 75
DB 668 TA-AGGAAGGACGACCTATCTCTCCGCAATCCACCAATTTTACAGCTATAAGGCAC 610
OY 76 IleThrTrpAsnThrTyrLysGluArgLeuValIleArgAlaLeuGluAsnArgValGly 95
DB ATAACTTAACAAACCTGGAAAGAACTCTGTAATCCAGGCTGTGAGACAAATTGGT 550
OY 96 IleTyrSerProHisThrAlaTyrAspAlaAlaProGluValAlaAsnAsnTrpLeuAla 115
DB ATGTATTTTCCCTACATAGACCTATGATGTCGACCCAGGAGGTTCGAACTGTGGCT 490
OY 116 LysGluLeuGlyAlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrPro 135
DB 489 AAAGGCTTGGAGCTTGGACCTGTAGCTGATGATCCCTTTCGAAAGCTTCCAGTCTCC 430
OY 136 ThrGluGlyAsnHisArgValGluIlePheAsnValAsnTyrThrGluAspLeuAspLysVal 155
DB 429 ATAGAG-----AACCC-AACGGAAGACCTGGACAAAGTTC 398
OY 156 MetSerAlaVal-LysGluIleAspGlyValSerValThrSerPheSerAlaArgThrGlu 175
DB 397 ACGTCTGAGTGAAAGAGGTTGTGAATGTCTGTGCGTCTTGTGTCTCCGAGGATGTA 338
```

```
RESULT 5
US-10-027-632-161387/c
; Sequence 161387, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161387
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161387

Alignment Scores:
Pred. No.: 1,87e-75 Length: 817
Score: 692.50 Matches: 175
Percent Similarity: 73.99% Conservative: 27
Best Local Similarity: 64.10% Mismatches: 60
Query Match: 38.49% Indels: 16
DB: 13 Gaps: 1

US-09-745-506-37 (1-350) x US-10-027-632-161387 (1-817)

OY 175 yAsnGluGlnThrArgIleAsnLeuAsnCysThrGluLysAlaLeuMetGluVal 195
DB ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 337
TGATGAAACAAACATGACTCAGCTCATGTTATCTACAGAGACTTGTGAGCAGTAGT 278
OY 195 lAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGlu 215
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 277
GGCTTTTCTCTCCAGACATATAAATGACATCAAGACTGAATTTATGTA-CTGGAGAA 219
OY 215 sProLeuLeuLeuHisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLe 235
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 218
GCCTTTGCTTACATATGATGGAATGGATGGTATGTCATGATGATGATGATCTCCCT 159
OY 235 uAlaThrMetIleAspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLe 255
DB 158 GACAGCCATGACTGAGTAATACACAGCCACTTAAACTATTACATATGTCCTTAGTCT 99
OY 255 uGlyValGlyArgThrLeuGlu-SerGluValLysValAlaLeuCysAlaGlySerG 275
DB 98 TAGAGTACGAGGACTGAGAGGTTCTTAAGTCAAAAGTCAGTGGCCCTGTGTCTGTCTG 39
OY 275 lYserSerValLeuGlnGlyValGluAlaAspLeu 286
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 38
GGAGAGGCTTCTGACAGATATAGAGCTGACCTT 4

RESULT 4
US-10-027-632-161386/c
; Sequence 161386, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161386
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161386

Alignment Scores:
Pred. No.: 1,87e-75 Length: 817
Score: 692.50 Matches: 175
Percent Similarity: 73.99% Conservative: 27
Best Local Similarity: 64.10% Mismatches: 60
Query Match: 38.49% Indels: 16
DB: 13 Gaps: 1

US-09-745-506-37 (1-350) x US-10-027-632-161386 (1-817)

OY 16 LeuserPheAlaGluSerTTrpAspAsnValGlyLeuValGluProSerProRoHis 35
DB CTCTATTGCTAAAGTTGTGACATATGAA-TTACTGGTGGAAACCAAGACATCAT 728
OY 36 ThrValAsnThrLeuPheLeuThrAsnAspLeuThrGluValMetGluValIleu 55
DB GCTATTAACACATC-TTCCAGACCAATGACTGAGGAGTGATGGAGAGGTGCTG 669
OY 56 GluIysLysAlaAspLeuIleLeuSerTyrHisProProIlePheArgProMetLysArg 75
DB 668 TA-AGGAAGGACGACCTATCTCTCCGCAATCCACCAATTTTACAGCTATAAGGCAC 610
OY 76 IleThrTrpAsnThrTyrLysGluArgLeuValIleArgAlaLeuGluAsnArgValGly 95
DB ATAACTTAACAAACCTGGAAAGAACTCTGTAATCCAGGCTGTGAGACAAATTGGT 550
OY 96 IleTyrSerProHisThrAlaTyrAspAlaAlaProGluValAlaAsnAsnTrpLeuAla 115
DB ATGTATTTTCCCTACATAGACCTATGATGTCGACCCAGGAGGTTCGAACTGTGGCT 490
OY 116 LysGluLeuGlyAlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrPro 135
DB 489 AAAGGCTTGGAGCTTGGACCTGTAGCTGATGATCCCTTTCGAAAGCTTCCAGTCTCC 430
OY 136 ThrGluGlyAsnHisArgValGluIlePheAsnValAsnTyrThrGluAspLeuAspLysVal 155
DB 429 ATAGAG-----AACCC-AACGGAAGACCTGGACAAAGTTC 398
OY 156 MetSerAlaVal-LysGluIleAspGlyValSerValThrSerPheSerAlaArgThrGlu 175
DB 397 ACGTCTGAGTGAAAGAGGTTGTGAATGTCTGTGCGTCTTGTGTCTCCGAGGATGTA 338
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; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 36054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 19746
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(480)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19746

Alignment Scores:
Pred. No.: 5.37e-58 Length: 480
Score: 548.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 30.46% Indels: 0
DB: 11 Gaps: 0

US-09-745-506-37 (1-350) x US-09-918-995-19746 (1-480)

QY 240 AsparaglyleuysarqhlslleuysleuSerhslleuqleuAlaLeuGlyValGlyArg 259
DB 50 GATCGAATTAATAAGACACCTTAATCTATTCCTTACGCTTACGCTTGGGCTGGGAGA 109
QY 260 ThrleuGluSerGluValAlaValAlaLeuGlyValGlySerGlySerValLeu 279
DB 110 ACCTTAGAGTCTCAAGCAAGCGTGGCCCTGTGTCTGTCTGTGGAGCAGCGCTCTG 169
QY 280 GluGlyValGluAlaAspLeuThrGlyGluMetSerhslleuysleuAspThrleuAsp 299
DB 170 CAGGCTGTGAGGTGACCTTACCTCAGAGTGATGCCCATCATGATATTTGGAT 229
QY 300 AlaAlaSerGluGlyIleAsnValIleLeuGlyGluHisSerAsnThrGluArgGlyPhe 319
DB 230 GCTGCTTCCCAAGGAATAATGTCATCTCTGTGACACACAGCACTGAACGAGGCTTT 289
QY 320 LeuSerAspLeuAlaGlyAspMetLeuAspSerhslleuGluAsnGlyIleAsnIleLeu 339
DB 290 CTTCCTGACCTTCGAGATATGCTGATTCCTCAGTGGAGAAATAATATATCTTA 349
QY 340 SerGluThrAspArgAspProLeuGluValVal 350
DB 350 TCAGAGACTGACAGGAGCCCTCTTCAGGTGGTA 382

RESULT 8
US-09-960-352-10848
; Sequence 10848, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO: 10848
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 46-LIB34-084-Q1-E1-D6
US-09-960-352-10848
```

```

Alignment Scores:
Pred. No.: 3.85e-48 Length: 394
Score: 467.00 Matches: 90
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 2
Query Match: 25.96% Indels: 0
DB: 10 Gaps: 0

US-09-745-506-37 (1-350) x US-09-960-352-10848 (1-394)

QY 1 MetAspLeuysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB 119 ATGATCTGAAGGCTCTCTTCCTTGAATGACTTTCATCCCTCATTTGCTGAG 178
QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProhslThrValAsnThrLeu 40
DB 179 AGCTGGACATATGTGATTACTGTGAAACGAGCCACACACACTGTAAACAGCTC 238
QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluGluIleLysAlaAsp 60
DB 239 TTCCTGACCAATGACTTGCATGAGAGATGATGAGAGAGCGCTGCAGAAAGAGCGGAT 298
QY 61 LeuIleLeuSerThrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
DB 299 CTCATCTCTCCCTACCATCCGCGCTATTTTCGACCATGAAGCGCATCAGCTGAAACA 358
QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsn 92
DB 359 TGAAGAGAGCGCCCTGTAAATCCGGGCACTGGAGAAC 394

RESULT 9
US-10-027-632-162668
; Sequence 162668, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 162668
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-162668

Alignment Scores:
Pred. No.: 1.1e-42 Length: 765
Score: 426.50 Matches: 103
Percent Similarity: 73.72% Conservative: 12
Best Local Similarity: 66.03% Mismatches: 31
Query Match: 23.71% Indels: 14
DB: 13 Gaps: 1

US-09-745-506-37 (1-350) x US-10-027-632-162668 (1-765)
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```

Db 2810 GATTATTAATTCGGAAGAACCCCACTATTTCGCCCACTTAAGCAGTTAACCAAGAT 2869
Oy 80 ThrtlygsluargheuvallleargalaleuglunargvalgllylserPro 99
Db 2870 AATTTCAGAAAGAAATGTRCGCTGATTTATTAACACAGATTTGCTGTTATGCGCG 2929
Oy 100 Hsthrlyalatyralalaproglnglyvalasnsrpleuallaysglyleugly 119
Db 2930 CATACTAACATGATTTATTTATGACAAATGGCTAAATGATGTTGTTGATATATGGGA 2989
Oy 120 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyProthnglylAsn 139
Db 2990 ATT-----AACAGACACACCTTTTAACATAA---ACA 3019
Oy 140 HisArgValGluPheAsn-----ValAsnTyThrGlnsPheAsnLysValMet 156
Db 3020 CATACGTTCCCTTAATAAAATTAAGCCGTTTGTGTCACATTAATGACGTCGCCAATG 3079
Oy 157 SerAlaValLysGlyLeaSpGlyVal-----SerValThrSerPhe 170
Db 3080 AGAGAGCTTTAGCTAGCTGCGCGCGGCTCAAGGTGATTTCTAAACAGATTAC 3139
Oy 171 Ser---AlaArgThrGlyAsnGluGlnThrArgLLeasnLysnCyThr----- 187
Db 3140 TCTTTAATTGGAACAGAGCTTTTACACCAACACA---GGACCAATCCACGATGGC 3196
Oy 188 -----GlnLysAlaLeuMetGlnValValAspPheLeuSer 199
Db 3197 GAAATTTGTCAGAAAGTGTCTGCAGAAAGCAAAATGACATGATTTTCCCTGAACCT 3256
Oy 200 ArgAsnLysGlnLeu-----TyrGlnLysThr----- 208
Db 3257 AAGCAGAACAAAGTCTTGACAGCTATGTACAGCGCAATCCCTTAAGAGAACGGGGTAT 3316
Oy 209 GlnLleLeuSerLeuLysProLeuLeuHisThrGlyMetGlyArgLysCysThr 228
Db 3317 GATGTTTATACCTTAATAAATCA---TCAAAAGAAATTTGCTTACGCGGTTGCGAGTA 3373
Oy 229 LeuAspGluSerValSerLeuAlaThrMetLleAspArgLLeysArgHisLeuLysLeu 248
Db 3374 TTGAGACAGCGCTGAGATTCTCTTATTTTGTACACCAAGTCAAGAGCTTCCCAATG 3433
Oy 249 SerHisLleArgLeuAlaLeuGlyValGlyArgThrLeuGlnSerGlnValLysValVal 268
Db 3434 GATGCTTCGCG-----KTCATTGCMAAAGATGACTAAATGATTCACAGGGTA 3484
Oy 269 AlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyVal-----GluAlaAsp 285
Db 3485 GCCATTGCTGGTGAAGTGGTGAATAATCTTATCATGATGATTCAGTAAACAGCGCAT 3544
Oy 286 LeuTyLLeuThrGlyLysMetSerHisHisAspThrLeuAspAlaLaseGlnGlyLle 305
Db 3545 GCTATATTAATCTGCTATGCTATTCATACGGCACATGATGATGCTGTAAGATTGA 3604
Oy 306 AsnValLle-----LeuCysGlnHisSerAsnThrGluArg 317
Db 3605 CCAGTTATGATCCTGCTGATTTACATTGAAGCGCTTTGT-----AAG 3646
Oy 318 GlyPheLeuSerAspLeuArgAspMetLeuAspSerHisLeuGlnLysnLleAsnLle 337
Db 3647 CCARAACTTGGAATTAATGAATCAATGAAACMAAATAATGATGCGGCTGATCCATT 3706
Oy 338 LleLeuSerGlnThrAspArgAspProLeuGln 348
Db 3707 TTGGAATCAGAAAGCAATACCAACCATTTTCGT 3739

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; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2452
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-2452

Alignment Scores:
Pred. No.: 3,62e-18 Length: 1140
Score: 230.00 Matches: 89
Percent Similarity: 44.35% Conservative: 72
Best Local Similarity: 24.52% Mismatches: 154
Query Match: 12.78% Indels: 48
DB: 10 Gaps: 13

US-09-745-506-37 (1-350) x US-09-738-626-2452 (1-1140)
Oy 17 SerPheAlaGluSerThrAspAsnValGlyLeuLeuValGluProSerProIleHisThr 36
Db 58 GCTTGGCGGAAAGCTGGGAGCAAGAGTGGGCTGATCTGC---GGTATCCACAGAGCTCG 114
Oy 37 ValAsnThrLeuPheLeuThrAsnAspLeuThrGlyLysValMetGlnGlyValLeuGln 56
Db 115 GTGAAGCGTCTCGATTACGACCTGATTCAGCCACCCAGCAAGCTGCCGCAAGGCTGTGAC 174
Oy 57 LysLysAlaAspLeuLeuSerTyHisProIlePheArgProMetLysArgLle 76
Db 175 ATGGGTTTGGACATGCTGATTCATTCACACCACTTCTGCTGCTGGGTGACCTGTT 234
Oy 77 ThrtPAsnThrTrpLysGluArgLeuValLleArgAlaLeuGlnAsnArgValGlyLle 96
Db 235 GCTGGGATGAGCCAAAGCAAGCTCATTCACACCTTATTCGGCGGGGGTGGCAGCTG 294
Oy 97 TyrSerProHisThrAlaTyAspAlaLleProGlnGlyValAsnAsnTrpLeuAlaLys 116
Db 295 TTTTCCGCGCACACTATTCGCGGATTCGCGCGCGCCAGGTGTCAACGATTAACTCGCCGAG 354
Oy 117 GlyLeuGlnLacysThrSerArgProIleHisProSerLysAlaProAsnTyProThr 136
Db 355 CTGCTGGCATCACAGCGCGCGGCGGCGCATGCGGCACAGCGCTTTAGCGGCATGAGACAA 414
Oy 137 GlnGlyAsnHisArgValGluPheAsnValAsnTyThrGlnsPheLeu-----AspLys 154
Db 415 TGGGGCGTGCAGCTTCTGCCCAAGAGTACGCGTAAAGAAAGATGCTTTGCAACGCA 474
Oy 155 ValMetSerAlaValLysGly-----LleAspGlyValSer--- 166
Db 475 GGTGCGGCTGCGATCGCGCACTACCGAGAGTGTGCTTTGAGATCGAAGACACCGGCGAG 534
Oy 167 -----ValThrSerPheSerAlaArgThrGlyAsnGluGlnThrArgLleAsn 183
Db 535 TTTAGCGCCCTGAGAGGGGGAGATCCGGCGACAGAGGGGACCTCGATTAG----- 582
Oy 184 LeuAsnCyThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysGln 203

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RESULT 13
US-09-738-626-2452
; Sequence 2452, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI

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Db 583 -----CTTTTAAATCCCTTGAGCTGCGCATCGAGTTTGTGGACCGCGCACTG 633
Qy 204 LeuTYrGlnLysThrGluIleLeu-----SerLeuGlnLysProLeuLeu--- 218
Db 634 CGGCGCCGCGCTACGCTGGGTGCTCGGAGGCTCATCCGATAGAGAGCCCTTCGAT 693
Qy 219 -----LeuHis-----ThrGlyMetGlyArgLeuGln 227
Db 694 ATTGTGAATGCACGCGCTGAGAGTTTAGAAATGCGACCGGATGGGTGGTGGT 753
Qy 228 ThrLeuAspGlnSerValSerLeuAlaThrMetIleAspArgIleLysArgHisLeuLys 247
Db 754 GAATTCGCGGAGCGGATCGCGCTCGGATTCGTGCAACAAGTGCCCAACACCTGCT 813
Qy 248 LeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr-----LeuGlnSerGlnVal 265
Db 814 GTCACCGCA-----TGGGGCGTGGCGCGCTACCGCGCATCTGAAACAATGGTG 861
Qy 266 LysValValAlaLeuGlnValGlySerGlySerSerValLeuGlnGlyVal----- 282
Db 862 TCCCGTGTGGGCTTTCATCAGGGTCCGAGTCTTAAACGATGTGATTAAGCTC 921
Qy 283 GluAlaAspLeuTYrLeuThrGlyGluMetSerHisAspThrLeuAspAlaLaser 302
Db 922 GGAGTGCAGCTTTATGTCACCTCTGATCTGCGCACATCCAGTTGATGAATCTCCGA 981
Qy 303 Gln---GlyIleAsnValIleLeuGlnSerGlnSerAsnThrGluArgGlyPheLeuSer 321
Db 982 GAAGTGGCCCTGCAGTATGATGATCTGCACACTGGCGCACGAAATTCATGAGCTTCC 1041
Qy 322 AspLeuArgAspMetLeu---AspSerHisLeuGlnLysIleAsnIleLeuSer 340
Db 1042 CAAGCCCAAGAAATTTGACAGACAAGCCCAAGGTTGAAGTTGATGATTCGATC 1101
Qy 341 GluThrAsp 343
Db 1102 CGCACAGAC 1110
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RESULT 14

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US-09-738-626-1/c
: Sequence 1, Application US/09738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIKOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIRO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, NAOKO
: APPLICANT: SENOH, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738,626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377484
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 00/280988
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: PatentIn ver. 3.0
: SEQ ID NO 1
: LENGTH: 3309400
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
: US-09-738-626-1
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Alignment Scores:

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Pred. No.: 1,2e-12 Length: 3309400
Score: 230.00 Matches: 89
Percent Similarity: 44.35% Conservative: 72
Best Local Similarity: 24.52% Mismatches: 154
Query Match: 12.78% Indels: 48
DB: 10 Gaps: 13

US-09-745-506-37 (1-350) x US-09-738-626-1 (1-3309400)
Qy 17 SerPheAlaGlnSerValSerPheAsnValGlyLeuLeuValGluProSerProProHisThr 36
Db 2374405 GCGTTGGCGGAAAGCTGGGCAAAAGTGGGTGATCTGCG---GGTATCCACAGAGCTCG 2374349
Qy 37 ValAsnThrLeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGln 56
Db 2374348 GTGAAGCGTGTGGGTTAGCATCTGATTCACCCAGGACAGTGGCCGCAAGGCTGTGGAC 2374289
Qy 57 LysLysAlaAspLeuIleLeuSerTYrHisProProIlePheArgProMetLysArgIle 76
Db 2374288 ATGGGTTTGGACATGCTGATCATTCACACCCATGCTGCTGGGTGGGTGACGTGCT 2374229
Qy 77 ThrThrAsnThrTrpLysGluArgLeuValIleArgAlaLeuGlnAsnArgValGlyIle 96
Db 2374228 GCTGGGATGAGCCAAAGGCAAGGATCATCACACCTTAATTCGCGCGGGGTGGCACTG 2374169
Qy 97 TYrSerProHisThrAlaTYrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLys 116
Db 2374168 TTTTCGCGGACACTAATGCGGATTCGCGCGCCAGGTGTCACAGATTAACCTGCCGAG 2374109
Qy 117 GlyLeuGlnAlaCysThrSerArgProIleHisProSerIlyAsaProAsnTYrProThr 136
Db 2374108 CTCGTGGCATCAGCGCGCGCGGCAACCATCCGACACGCGCTTTAGCGGCATGACAAA 2374049
Qy 137 GluGlnAsnHisArgValGluPheAsnValAsnTYrThrGlnAspLeu-----AspLys 154
Db 2374048 TGGGGCGTGCACGTTCTGCCCAAGATGCACGATCACTAAAGAGATGCTTTTCGAGCA 2373989
Qy 155 ValMetSerAlaValLysGly-----IleAspGlyValSer--- 166
Db 2373988 GGTGGCGGTGGATCGCGGACTACCGAGAGTGTGCTTTAGAGTGAAGTGAAGACCGGCGAG 2373929
Qy 167 -----ValThrSerPheSerAlaArgThrGlnGlnGluGlnArgIleAsn 183
Db 2373928 TTTAGCGCCGTGGAGGGGCGCAATCCGGCAGAGGGGAGCGATGAAG----- 2373881
Qy 184 LeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysGln 203
Db 2373880 -----CTTTTAAATCCCTTGAGCTGCGCATCGAGTTGTTGTCACCGCGCAACTG 2373830
Qy 204 LeuTYrGlnLysThrGluIleLeu-----SerLeuGlnLysProLeuLeu--- 218
Db 2373829 CGCGCCGCGCTACGCTGGGTGCTCGGAGGCTCATCCGATAGAGAGCCCTTCGAT 2373770
Qy 219 -----LeuHis-----ThrGlyMetGlyArgLeuGln 227
Db 2373769 ATTGTGAATGCACGCGCTGAGAGTTTAGAAATGCGACCGGATGGGTGGTGGT 2373710
Qy 228 ThrLeuAspGlnSerValSerLeuAlaThrMetIleAspArgIleLysArgHisLeuLys 247
Db 2373709 GAATTCGCGGAGCGGATCGCGCTCGGATTCGTGCAACAAGTGCCCAACACCTGCT 2373650
Qy 248 LeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr-----LeuGlnSerGlnVal 265
Db 2373649 GTCACCGCA-----TGGGGCGTGGCGCGCTACCGCGCATCTGAAACAATGGTG 2373602
Qy 266 LysValValAlaLeuGlnValGlySerGlySerSerValLeuGlnGlyVal----- 282
Db 2373601 TCCCGTGTGGGCTTTCATCAGGGTCCGAGTCTTAAACGATGTGATTAAGCTC 2373542
Qy 283 GluAlaAspLeuTYrLeuThrGlyGluMetSerHisAspThrLeuAspAlaLaser 302
Db 2373541 GGAGTGCAGCTTATGTCATCTGATCTGCGCACACATCCAGTTGATGAATATCTCCGA 2373482
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